

SEQUENCE LISTING

<110> Irie, Reiko
 Tsunoda, Hiroyuki
 Igawa, Tomoyuki
 Sekimori, Yasuo
 Tsuchiya, Masayuki

<120> IgM PRODUCTION BY TRANSFORMED CELL AND
 METHOD OF QUANTIFYING THE SAME

<130> 14875-155US1

<150> PCT/JP2004/010444

<151> 2004-07-15

<150> US 60/487,333

<151> 2003-07-15

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<400> 1

atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt	48
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly	
1 5 10 15	
gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag	96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln	
20 25 30	
cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt	144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
35 40 45	
agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg	192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca	240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala	
65 70 75 80	
gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac	288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn	
85 90 95	

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala 115 120 125	384
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala 130 135 140	432
cca acc ctt ttc ccc ctg gtc tcc tgt gag aat tcc ccg tcg gat acg Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr 145 150 155 160	480
agc agc gtg gcc gtt ggc tgc ctg gca cag gac ttc ctt ccc gac tcc Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser 165 170 175	528
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr 180 185 190	576
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser 195 200 205	624
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His 210 215 220	672
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val 225 230 235 240	720
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val 245 250 255	768
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctg atc Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile 260 265 270	816
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu 275 280 285	864
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln 290 295 300	912
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr 305 310 315 320	960

ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc	1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys	
325 330 335	
cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg	1056
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met	
340 345 350	
tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca	1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro	
355 360 365	
tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg	1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu	
370 375 380	
gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc	1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg	
385 390 395 400	
cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac	1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His	
405 410 415	
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat	1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp	
420 425 430	
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac	1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp	
435 440 445	
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc	1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala	
450 455 460	
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg	1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu	
465 470 475 480	
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct	1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser	
485 490 495	
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc	1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser	
500 505 510	
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca	1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro	
515 520 525	
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg	1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp	
530 535 540	
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc	1680

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro	
545 550 555 560	
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc	1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr	
565 570 575	
ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac	1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr	
580 585 590	
tga	1779
<210> 2	
<211> 592	
<212> PRT	
<213> Homo sapiens	
<400> 2	
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly	
1 5 10 15	
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln	
20 25 30	
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
35 40 45	
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala	
65 70 75 80	
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn	
85 90 95	
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
100 105 110	
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala	
115 120 125	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala	
130 135 140	
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr	
145 150 155 160	
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser	
165 170 175	
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr	
180 185 190	
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser	
195 200 205	

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
 210 215 220
 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
 225 230 235 240
 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
 245 250 255
 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
 260 265 270
 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
 275 280 285
 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
 290 295 300
 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
 305 310 315 320
 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
 325 330 335
 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
 340 345 350
 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
 355 360 365
 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
 370 375 380
 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
 385 390 395 400
 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
 405 410 415
 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
 420 425 430
 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
 435 440 445
 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
 450 455 460
 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
 465 470 475 480
 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
 485 490 495
 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
 500 505 510

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
530 535 540

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545 550 555 560

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
565 570 575

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
580 585 590

<210> 3
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(723)

<400> 3
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15
ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45
gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95
ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc 384
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr

115	120	125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc			432
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe			
130	135	140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc			480
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg			528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			
	165	170	175
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag			576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			
	180	185	190
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc			624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser			
	195	200	205
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat			672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			
	210	215	220
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt			720
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	240
tag			723
<210> 4			
<211> 240			
<212> PRT			
<213> Homo sapiens			
<400> 4			
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser			
1	5	10	15
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala			
	20	25	30
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser			
	35	40	45
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
	50	55	60
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
65	70	75	80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
	85	90	95
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr			

100								105				110				
Tyr	Cys	Gln	Gln	Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	
115				120				125								
Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	
130				135				140								
Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	
145				150				155				160				
Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	
165				170				175								
Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	
180				185				190								
Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
195				200				205								
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	
210				215				220								
Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
225				230				235				240				
<210> 5																
<211> 480																
<212> DNA																
<213> Homo sapiens																
<220>																
<221> CDS																
<222> (1)..(480)																
<400> 5																
atg	aag	aac	cat	ttg	ctt	ttc	tgg	gga	gtc	ctg	gcg	gtt	ttt	att	aag	48
Met	Lys	Asn	His	Leu	Leu	Phe	Trp	Gly	Val	Leu	Ala	Val	Phe	Ile	Lys	
1	5			10				15								
gct	gtt	cat	gtg	aaa	gcc	caa	gaa	gat	gaa	agg	att	gtt	ctt	gtt	gac	96
Ala	Val	His	Val	Lys	Ala	Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp	
20				25				30								
aac	aaa	tgt	aag	tgt	gcc	cgg	att	act	tcc	agg	atc	atc	cgt	tct	tcc	144
Asn	Lys	Cys	Lys	Cys	Ala	Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser	Ser	
35				40				45								
gaa	gat	cct	aat	gag	gac	att	gtg	gag	aga	aac	atc	cga	att	att	gtt	192
Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	Val	
50				55				60								
cct	ctg	aac	aac	agg	gag	aat	atc	tct	gat	ccc	acc	tca	cca	ttg	aga	240
Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	
65				70				75				80				

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct 288
 Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
 85 90 95

aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336
 Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
 100 105 110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga 384
 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
 115 120 125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432
 Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
 130 135 140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa 480
 Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 145 150 155

<210> 6
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
 1 5 10 15

Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30

Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
 50 55 60

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
 65 70 75 80

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
 85 90 95

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
 100 105 110

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
 115 120 125

Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
 130 135 140

Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 145 150 155

<210> 7

<211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized sequence

 <400> 7
 ccaacggcaa caaagaaaag aacg 24

 <210> 8
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized sequence

 <400> 8
 aacatgctct ggccgagcca gtcg 24

 <210> 9
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized sequence

 <400> 9
 gcaagtcag ccagagtgtt ttat 24

 <210> 10
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized sequence

 <400> 10
 ctgtccttgc tgtcctgctc tgtg 24

 <210> 11
 <211> 33
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized primer sequence

 <400> 11
 aacagctcga gccaccatgg agtttgggct gag 33

 <210> 12
 <211> 32
 <212> DNA

<213> Artificial
 <220>
 <223> an artificially synthesized primer sequence
 <400> 12
 agcggccagc cgccccgagc ctgtcgacag gc 32
 <210> 13
 <211> 32
 <212> DNA
 <213> Artificial
 <220>
 <223> an artificially synthesized primer sequence
 <400> 13
 atagaattcc accatggtgt tgcagaccca gg 32
 <210> 14
 <211> 30
 <212> DNA
 <213> Artificial
 <220>
 <223> an artificially synthesized primer sequence
 <400> 14
 ggagcaggcg gccgcacttc tccctctaac 30
 <210> 15
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <223> an artificially synthesized sequence
 <400> 15
 accattgaga accagatttg tgta 24
 <210> 16
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <223> an artificially synthesized sequence
 <400> 16
 tgtgtagcac ttgtttctgt cata 24
 <210> 17
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 17
 atgaattcca ccatgaagaa ccatttgc 28

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 18
 tatctagatt agtcaggata gcaggc 26

<210> 19
 <211> 1788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1788)

<400> 19
 atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt 48
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
 1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag 96
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
 Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

gag tgg gtc tca gct att agt ggt agt ggt tat acc aca tac tac gca 240
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala
 65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 288
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

tat tac tgt gcc aaa aaa ccg ggg gac tat ggt tcg ggg agt tat tac 384

Tyr	Tyr	Cys	Ala	Lys	Lys	Pro	Gly	Asp	Tyr	Gly	Ser	Gly	Ser	Tyr	Tyr	
		115					120					125				
ctt	gac	tac	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	432
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	
	130					135					140					
gca	tcc	gcc	cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	480
Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	
145					150					155					160	
tcg	gat	acg	agc	agc	gtg	gcc	gtt	ggc	tgc	ctc	gca	cag	gac	ttc	ctt	528
Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	
				165				170						175		
ccc	gac	tcc	atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	576
Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile	
			180					185					190			
agc	agc	acc	cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	624
Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	
		195					200				205					
gcc	acc	tca	cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	672
Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	
	210					215					220					
gac	gaa	cac	gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	720
Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	
225					230					235					240	
aag	aac	gtg	cct	ctt	cca	gtg	att	gct	gag	ctg	cct	ccc	aaa	gtg	agc	768
Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	
				245				250						255		
gtc	ttc	gtc	cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	816
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	
			260				265					270				
aag	ctc	atc	tgc	cag	gcc	acg	ggt	ttc	agt	ccc	cgg	cag	att	cag	gtg	864
Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	
		275					280					285				
tcc	tgg	ctg	cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	912
Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	
	290					295					300					
cag	gtg	cag	gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	960
Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	
305					310					315					320	
acc	agc	aca	ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	agc	cag	agc	atg	1008
Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser	Gln	Ser	Met	
				325					330					335		
ttc	acc	tgc	cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	1056
Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	

340	345	350	
tcc tcc atg tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala 355 360 365			1104
atc ccc cca tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu 370 375 380			1152
acc tgc ctg gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser 385 390 395 400			1200
tgg acc cgc cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser 405 410 415			1248
gag agc cac ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile 420 425 430			1296
tgc gag gat gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr 435 440 445			1344
cac aca gac ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys 450 455 460			1392
ggg gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg 465 470 475 480			1440
gag cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr 485 490 495			1488
ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln 500 505 510			1536
ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro 515 520 525			1584
cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu 530 535 540			1632
gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu 545 550 555 560			1680
gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly 565 570 575			1728

```

aaa ccc acc ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc      1776
Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
                    580                      585                      590

acc tgc tac tga
Thr Cys Tyr
                    595

<210> 20
<211> 595
<212> PRT
<213> Homo sapiens

<400> 20
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1                    5                      10                      15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
                20                      25                      30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    35                      40                      45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                      55                      60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala
65                      70                      75                      80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                      90                      95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
    100                      105                      110

Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr
    115                      120                      125

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser
    130                      135                      140

Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro
145                      150                      155                      160

Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu
                165                      170                      175

Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile
    180                      185                      190

Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala
    195                      200                      205

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr
    210                      215                      220

```

Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	225	230	235	240
Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	245	250	255	
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	260	265	270	
Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	275	280	285	
Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	290	295	300	
Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	305	310	315	320
Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser	Gln	Ser	Met	325	330	335	
Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	340	345	350	
Ser	Ser	Met	Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg	Val	Phe	Ala	355	360	365	
Ile	Pro	Pro	Ser	Phe	Ala	Ser	Ile	Phe	Leu	Thr	Lys	Ser	Thr	Lys	Leu	370	375	380	
Thr	Cys	Leu	Val	Thr	Asp	Leu	Thr	Thr	Tyr	Asp	Ser	Val	Thr	Ile	Ser	385	390	395	400
Trp	Thr	Arg	Gln	Asn	Gly	Glu	Ala	Val	Lys	Thr	His	Thr	Asn	Ile	Ser	405	410	415	
Glu	Ser	His	Pro	Asn	Ala	Thr	Phe	Ser	Ala	Val	Gly	Glu	Ala	Ser	Ile	420	425	430	
Cys	Glu	Asp	Asp	Trp	Asn	Ser	Gly	Glu	Arg	Phe	Thr	Cys	Thr	Val	Thr	435	440	445	
His	Thr	Asp	Leu	Pro	Ser	Pro	Leu	Lys	Gln	Thr	Ile	Ser	Arg	Pro	Lys	450	455	460	
Gly	Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro	Pro	Ala	Arg	465	470	475	480
Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys	Leu	Val	Thr	485	490	495	
Gly	Phe	Ser	Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln	Arg	Gly	Gln	500	505	510	
Pro	Leu	Ser	Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	Pro	515	520	525	

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
530 535 540

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
545 550 555 560

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
565 570 575

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
580 585 590

Thr Cys Tyr
595

<210> 21
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(726)

<400> 21
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

aaa cca gga cag cct cct aag ttg ctc att tac tgg gca tct acc cgg 240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

tac tgt cag caa tat tat act act ctt ccg ctc act ttc ggc gga ggg 384
Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
115 120 125

acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc 432
 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 130 135 140

ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg 480
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 145 150 155 160

tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag 528
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 165 170 175

gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag 576
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 180 185 190

cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg 624
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 195 200 205

agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc 672
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 210 215 220

cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag 720
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 225 230 235 240

tgt tag 726
 Cys

<210> 22
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly
 115 120 125
 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 130 135 140
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 145 150 155 160
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 165 170 175
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 180 185 190
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 195 200 205
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 210 215 220
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 225 230 235 240

Cys

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 23
 caacaggcag gcaggggcag caag

24

<210> 24
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 24
 agcataatta aagccaagga ggag

24

<210> 25
 <211> 68
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized sequence

<400> 25
 cctgatcatg aagacgtcga ctagtccgga tccccgggag ctcgagcgct ctagatcttt 60
 aattaagg 68

<210> 26
 <211> 76
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized sequence

<400> 26
 cgcgcccttaa ttaaagatct agagcgctcg agtccccggg gatccggact agtcgacgtc 60
 ttcgatgatca ggccgg 76

<210> 27
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 27
 gaggaattcc accatgaaga acc 23

<210> 28
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 28
 gaggcggccg cttagtcagg atagcag 27

<210> 29
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer sequence

<400> 29
 aaaagcggcc gcgatcataa tcagccatac ca 32

<210> 30
 <211> 36
 <212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 30

aaaactcgag aagcttagac atgataagat acattg

36

<210> 31

<211> 12

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized linker sequence

<400> 31

cccggatccg gg

12